

1/21  
**FcR-I**

1	GCAGGAATTGGCACGGCTCTGTCTGCCAGCACGGAGGGCTATCCATCCACAGAGC	60
61	AGTGCAGTGGGAGGAGACGCCATGACCCCCATCCTCACGGTCTGATCTGTCTGGGCC	120
1	M T P I L T V L I C L G P	13
121	CTCCCCAAGCCCACCCCTCTGGGCTGAGCCAGGCTCTGTGATCACCAAGGGAGTCCTGTG	180
14	L P K P T L W A E P G S V I T Q G S P V	33
181	ACCTCAGGTGTCAGGGAGCCTGGAGACGCAGGAGTACCATCTATATAGAGAAAAGAAA	240
34	T L R C Q G S L E T Q E Y H L Y R E K K	53
241	ACAGCACTCTGGATTACACGGATCCCACAGGAGCTGTGAAGAAGGGCCAGTTCCCATC	300
54	T A L W I T R I P Q E L V K K G Q F P I	73
301	CTATCCATCACCTGGAACATGCAGGGCGGTATTGCTGTATCTATGGCAGCCACACTGCA	360
74	L S I T W E H A G R Y C C I Y G S H T A	93
361	GGCCTCTCAGAGAGCAGTGACCCCTGGAGCTGGTGGTACAGGAGCCTACAGCAAACCC	420
94	G L S E S S D P L E L V V T G A Y S K P	113
421	ACCTCTCAGCTCTGCCAGCCCTGTGGTACCTCAGGAGGAAATGTGACCATCCAGTGT	480
114	T L S A L P S P V V T S G G N V T I Q C	133
481	GACTCACAGGTGGCATTGATGGCTTCATTCTGTGTAAGGAAGGAGAAGATGAACACCCA	540
134	D S Q V A F D G F I L C K E G E D E H P	153
541	CAATGCCTGAACCTCCATTCCATGCCCGTGGTCATCCGGGCCATCTCTCCGTGGC	600
154	Q C L N S H S H A R G S S R A I F S V G	173
601	CCCGTGAGCCCAAGTCGCAGGTGGTCGTACAGGTGCTATGGTTATGACTCGCGCGCTCCC	660
174	P V S P S R R W S Y R C Y G Y D S R A P	193
661	TATGTGTGGTCTCTACCCAGTGATCTCTGGGCTCTGGTCCCAGGTGTTCTAAGAAG	720
194	Y V W S L P S D L L G L L V P G V S K K	213
721	CCATCACTCTCAGTGCAGCCGGTCCTGTCGTGGCCCTGGGGAGAAGCTGACCTCCAG	780

**FIG. 1A**

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**FcR-I**

214	P S L S V Q P G P V V A P G E K L T F Q	233
781	TGTGGCTCTGATGCCGGCTACGACAGATTGTTCTGTACAAGGAGTGGGGACGTGACTTC	840
234	C G S D A G Y D R F V L Y K E W G R D F	253
841	CTCCAGCGCCCTGGCCGGCAGCCCCAGGCTGGCTCTCCAGGCCAACTTCACCCCTGGC	900
254	L Q R P G R Q P Q A G L S Q A N F T L G	273
901	CCTGTGAGCCGCTCCTACGGGGGCCAGTACACATGCTCCGGTGCATAAACCTCTCC	960
274	P V S R S Y G G Q Y T C S G A Y N L S S	293
961	GAGTGGTCGGCCCCCAGCGACCCCTGGACATCCTGATCACAGGACAGATCCGTGCCAGA	1020
294	E W S A P S D P L D I L I T G Q I R A R	313
1021	CCCTTCCCTCCGTGGGCCGGCCCCACAGTGGCCTCAGGAGAGAACGTGACCCCTGCTG	1080
314	P F L S V R P G P T V A S G E N V T L L	333
1081	TGTCAGTCACAGGGAGGGATGCACACTTCCTTTGACCAAGGAGGGCAGCTGATTCC	1140
334	C Q S Q G G M H T F L L T K E G A A D S	353
1141	CCGCTGCGTCTAAATCAAAGCGCCAATCTCATAAGTACCAGGCTGAATTCCCCATGAGT	1200
354	P L R L K S K R Q S H K Y Q A E F P M S	373
1201	CCTGTGACCTCGGCCACGCGGGGACCTACAGGTGCTACGGCTCACTCAGCTCCAACCC	1260
374	P V T S A H A G T Y R C Y G S L S S N P	393
1261	TACCTGCTGACTCACCCAGTGACCCCTGGAGCTCGTGGTCTCAGGAGCAGCTGAGACC	1320
394	Y L L T H P S D P L E L V V S G A A E T	413
1321	CTCAGCCCACCAAAACAAGTCCGACTCCAAGGCTGGTGAGTGAGGAGATGCTTGGCGT	1380
414	L S P P Q N K S D S K A G E *	427
1381	GATGACGCTGGGCACAGAGGGTCAGGTCTGTCAAGAGGGAGCTGGGTGTCCTGGTGGAC	1440
1441	ATTTGAAGAATTATTCATTCCAACTTGAAGAATTATTCAACACCTTAACAATGTATA	1500
1501	TGTGAAGTACTTATTCTTCATATTTAAAAATAAAAGATAATTATCCATG	1552

**FIG. 1B**

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Percent Similarity: 63.090

Percent Identity: 45.064

**HMQDO20.aa x FCg2RBos.aa**

191 RAPYVWSLPSDLLGLLVPGVSKPKSLSVQPGPVAPGEKLTQCGSDAGY 240

.| ..::|.| . :| . : :| . || : .::|:||:| . .::|:| . .::|

6 PALLCLGLS VGLRTQVQAGTFPKPIIWAEPSSV VPLGSSVTILCQGPPNT 55

241 DRFVLYKEWGRDFLQRPG RQ P QAGLSQANFTLGPVSR SYGGQYTC SGAYN 290

..| | | | | | . : . . . . . . || | :| . :| . | | | .

56 KSFSLNKE..GDSTPWNIHPSLEPWDKANFFFISNVREQQAGRYHCS..HF 101

291 LSSEWSAPSDPLDILITGQ.....IRARPFLSVRPGPTVASGENVTLLCQ 335

:: :||.||:|||:||.||: . :| .|| | |||:||.||.|||1|||1|||

102 IGVNWSEPSEPLDLLVAGEEPAGRLRDRPSLSVRPSPS VAPGENVTLLCQ 151

336 SQGGMHTFLLTKEGAADSPRLKSKRQSHKYQAEFPMS PVTSAHAGTYRC 385

|.. .||||.|||||..||||:|. |. .|||||. :|||||||:|||||

152 SGNRTDTFLLSKEGA AHRPLRLRSQDQDGWYQAEFSLS PVTSAHGGTYRC 201

386 YGSLSNPYLLTHPSDPLELVVSG.....AAETL.....SP 416

| |||.|||||. :|||:||.||:| . : . ||..| . :| .

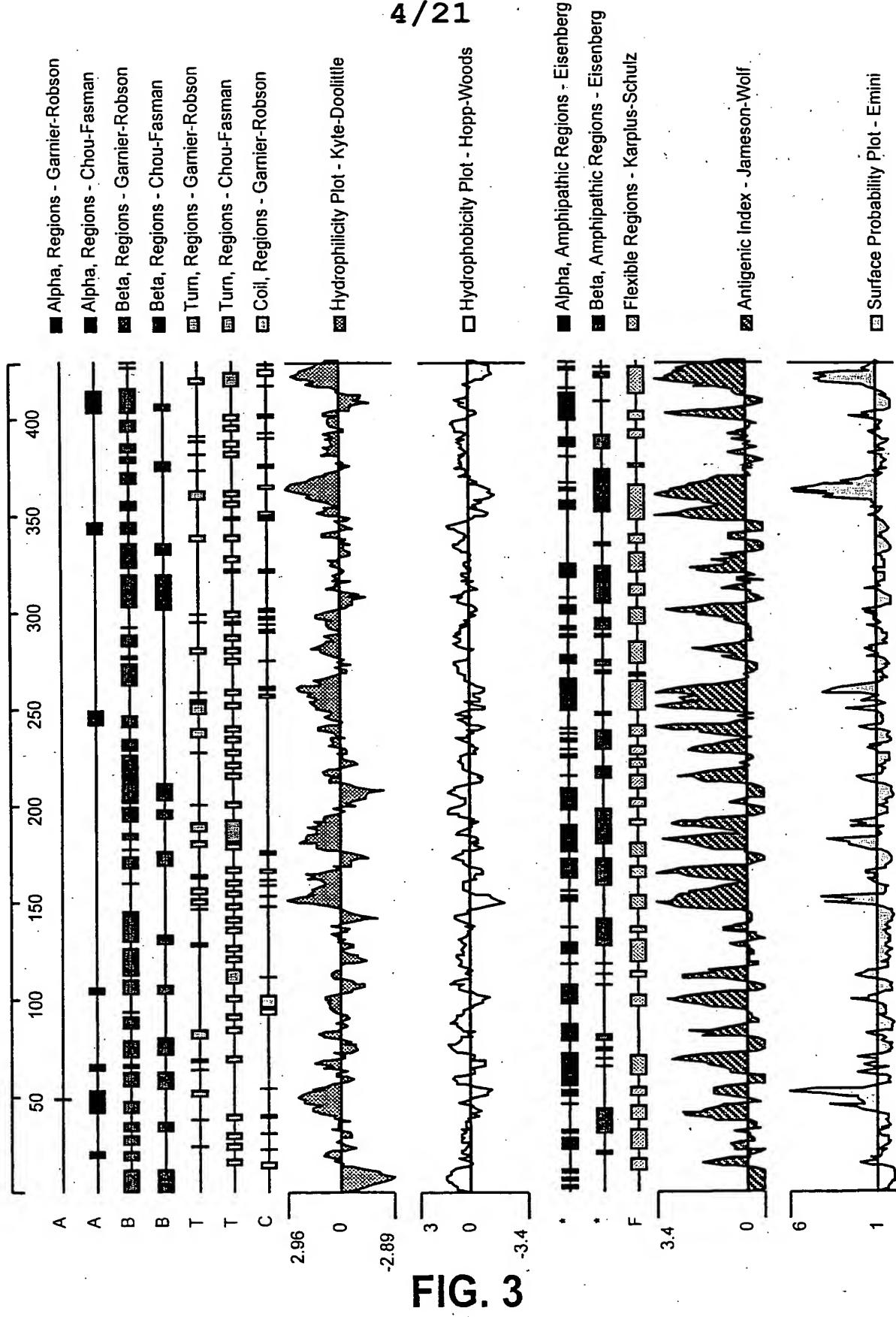
202 YRSLSTNPYLLSQPSEPL ALLVADYTMQNLIRMG LAASV LLLGILLCQA 251

417 PQNKSDSKAGE 427

.::: .::: .:::

252 RHDHGGAREAA 262

**FIG. 2**



## FcRII

1	ACCCACGCGTCCGCACTCTAGCGGTATCTGCCACCATGGCCCTGGTGCTGATCCTCCAG	60
1	<u>M A L V L I L O</u>	8
61	CTGCTGACCCCTCTGGCCTCTGTGTCACACAGACATCACTCCGTCTGTCCCCCAGCTTCA	120
9	<u>L L T L W P L C H T D I T P S V P P A S</u>	28
121	TACCACCCCTAACGCCATGGCTGGGAGCTCAGCCGGCTACAGTTGTGACCCCTGGGTCAAC	180
29	<u>Y H P K P W L G A Q P A T V V T P G V N</u>	48
181	GTGACCTTGAGATGCCGGGACCCCCAACCGCTTGGAGATTGGACTTTCAAGCCTGG	240
49	<u>V T L R C R A P Q P A W R F G L F K P G</u>	68
241	GAGATCGCTCCCTTCTCTCCGGGATGTGTCCTCCGAGCTGGCAGAATTCTTCTGGAG	300
69	<u>E I A P L L F R D V S S E L A E F F L E</u>	88
301	GAGGTGACTCCAGCCAAGGGGGAAAGTTACCGCTGCTGCTACCGAAGGCCAGACTGGGG	360
89	<u>E V T P A Q G G S Y R C C Y R R P D W G</u>	108
361	CCGGGTGTCTGGTCCCAGCCAGCGATGTGTCCTGGAGCTGCTGGTACAGAGGAGCTGCCG	420
109	<u>P G V W S Q P S D V L E L L V T E E L P</u>	128
421	CGGCCGTCGCTGGTGGCGCTGCCGGGGCGGTGGTGGTCCCTGGCGCCAACGTGAGCCTG	480
129	<u>R P S L V A L P G P V V G P G A N V S L</u>	148
481	CGCTGCGGGCCGCTGCGAACATGAGCTCGTCTGCTGACCCGAGGGCGTGGCGGC	540
149	<u>R C A G R L R N M S F V L Y R E G V A A</u>	168
541	CCGCTGCAGTACCGCCACTCCGCGCAGCCCTGGGCCGACTTCACGCTGCTGGCGCCCGC	600
169	<u>P L Q Y R H S A Q P W A D F T L L G A R</u>	188
601	GCCCCCGGCACCTACAGCTGCTACTATCACACGCCCTCCGCGCCCTACGTGCTGTCGCAG	660
189	<u>A P G T Y S C Y Y H T P S A P Y V L S Q</u>	208

FIG. 4A

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**FcRII**

661	CGCAGCGAGGTGCTGGTCATCAGCTGGGAAGACTCTGGCTCCTCCGACTACACCCGGGG	720
209	R S E V L V I S W E D S G S S D Y T R G	228
721	AACCTAGTCGCGCTGGGGCTGGCCGGGCTGGTCCTCATCTCCCTGGCGCGCTGGTCACT	780
229	N L V R L G L A G L V L I S L G A L V T	248
781	TTTGAATGGCCGACTCAGAACCGCGCTCTGCTGGTATCCGCCCTGAGCCCCAGGAGCA	840
249	F D W R S Q N R A P A G I R P *	263
841	CTGCAGCCCGAGACTTCAACCTGAGTGGCGGAGAAGCTGGGACCCCTGGGCTGGACTGTC	900
901	CTTTCCTGCAGCCCCACAGTCCTGCTGGCTGAGCTCCGCGAACGGTCCTTAGACCCCGC	960
961	TGTGCCCTGTGCTGTAGCTTCTTCCAGGCCTTCCAAGGAGTAGCTGAAAGGAAGACG	1020
1021	CGATTAGTGGTTAAGACTTCAAGCCAGAACAGACAGAGGGTTCGAATCCCAGCACTGCCGT	1080
1081	CTACTCACTGTAGTAGCTAGCAGCTACAGAAAGGTAGTAGTGAGACGTGAAGCCAGCTGGA	1140
1141	CTTCCTGGGTTGAATGGGGACCTGGAGAACCTTCTGTCTTACAAGAGGATTGTAAAATG	1200
1201	GACCAATCAGCACTCTGTAAGATGGACCAATCAGCGCTCTGTAAAATGGACCAATCAGCA	1260
1261	GGACATGGCGGGGACAATAAGGAATAAAAGCTGGCGAGCGCGGCACCCACCAGAGTC	1320
1321	TGCTTCCACGCTGTGGGAGCTTGTCTTGCTCTACACAATAATCTGCTGCTGCTA	1380
1381	AAAAAAAAAAAAAAAAAAAAAA	1410

**FIG. 4B**

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Percent Similarity: 54.400

Percent Identity: 37.600

HDPMK33.aa x FCg2RBos.aa

5 LILQLLTLWPLCHTDITPSVPPASYHPKPWLGAQPATVVTPGVNVTLCR 54

1 MAPTLPALLCLGLSGLRTQVQAGTFPKPIIWAEPSSVVPLGSSVTILCQ 50

55 APQPAWRFGLFKPGEIAPLLFRDV..SSELAEFFLEEVTPAQGGSYRCCY 102

.;. ....|.;| |.;|: ;|: ;|: ..| ;|:|;|:|:| ..|;|:|.;|:|:

51 GPPNTKSFSLNKEGSTPWNIIHPSLEPWDKANFFISNVREQQAGRYHCS. 99

103 RRPDWGPGVWSQPSDVLELLVTEELP.....RPSLVALPGPVVGPGANV 146

100 ...HFIGVNWSEPSEPLDLLVAGEEPAGRLDRPSLSVRPSPSVAPGENV 146

147 SLRCAGRLRNMSFVLYREGVAA. PLOQRHSAQP...WADFTL..LGARAP 190

147 TLLCOSGNRTDTFLLSKEGAHRPLRLRSQDQDGWYQAEFSLSPVTSAGH 196

191 GTYSCYYHTPSAPVLSQRSEVLVISWEDSGSSDYTRGNLVRGLAGLVL 240

197 GTYRCYRSLSTNPYLLSOPSEPLALL....VADYTMONLIRMGGLAASVL 241

241 ISLGALVTFDWRSONRAPAGIRP 263

242 LIGLI COARHDHGGAAREAARS 264

**FIG. 5**

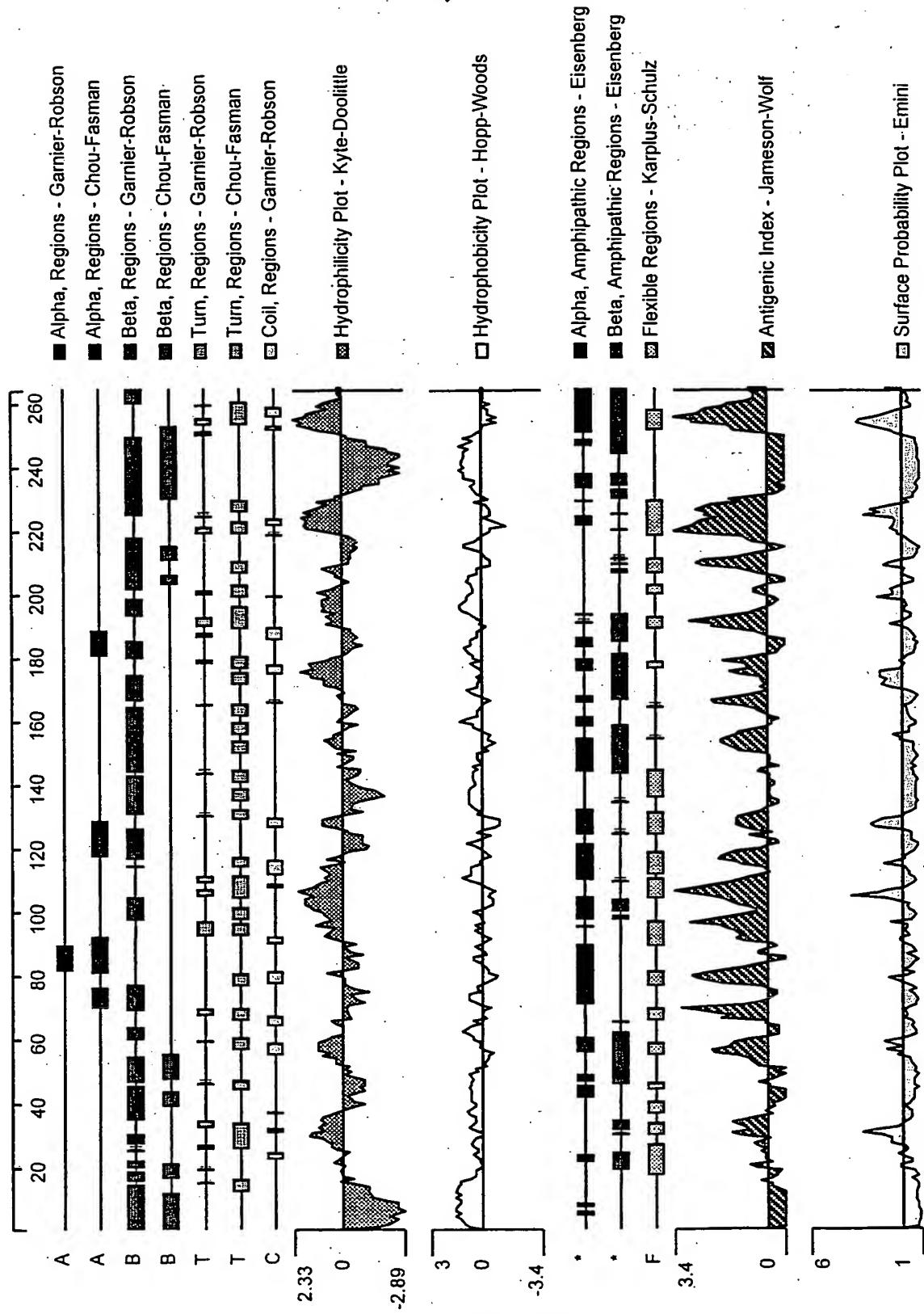


FIG. 6

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**FCR-III**

1 GCAGGAATTGGCACGAGCAGCACTGAGGGCTCATCCCTCTGCAGAGCGCGGGGTCACCG 60  
61 GAAGGAGACGCCATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGCTGAGTCTGGC 120  
1 M T P A L T A L L C L G L S L G 16  
121 CCCAGGACCCGCGTGCAGGCAGGGCCCTTCCCCAAACCCACCCCTCTGGCTGAGCCAGGC 180  
17 P R T R V Q A G P F P K P T L W A E P G 36  
181 TCTGTGATCAGCTGGGGAGCCCCGTGACCATCTGGTGTAGGGAGCCTGGAGGCCAG 240  
37 S V I S W G S P V T I W C Q G S L E A Q 56  
241 GAGTACCAACTGGATAAAGAGGGAAAGCCCAGAGCCCTGGACAGAAATAACCCACTGGAA 300  
57 E Y Q L D K E G S P E P L D R N N P L E 76  
301 CCCAAGAACAAAGGCCAGATTCTCCATCCATCCATGACACAGCACCATGCAGGGAGATA 360  
77 P K N K A R F S I P S M T Q H H A G R Y 96  
361 CGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCAGCGACCCCTGGAGCTGGT 420  
97 R C H Y Y S S A G W S E P S D P L E L V 116  
421 ATGACAGGGAGCCTATAGCAAACCCACCCCTCTCAGCCCTGCCAGCCCTGTGGTGCCTCA 480  
117 M T G A Y S K P T L S A L P S P V V A S 136  
481 GGGGGGAATATGACCCCTCGATGTGGTCACAGAAGAGATATCACCATTGTTCTGATG 540  
137 G G N M T L R C G S Q K R Y H H F V L M 156  
541 AAGGAAGGGAGAACACCAGCTCCCCGGACCCCTGGACTCACAGCAGCTCCACAGTGGGGG 600  
157 K E G E H Q L P R T L D S Q Q L H S G G 176  
601 TTCCAGGCCCTGTTCCCTGTGGCCCCGTGAACCCACAGGCCACAGGTGGAGGTTACATGC 660  
177 F Q A L F P V G P V N P S H R W R F T C 196

**FIG. 7A**

## FcR-III

661	TATTACTATTATGAAACACCCCCCGGGTGTGGTCCCACCCAGTGACCCCTGGAGATT	720
197	Y Y Y Y M N T P R V W S H P S D P L E I	216
721	CTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCCCTGCAGGGCCCTGTCCCTGGCC	780
217	L P S G V S R K P S L L T L Q G P V L A	236
781	CCTGGGCAGAGCCTGACCCCTCCAGTGTGGCTCTGATGTGGCTACGACAGATTGTTCTG	840
237	P G Q S L T L Q C G S D V G Y D R F V L	256
841	TATAAGGAGGGGAACGTGACTTCCCTCCAGGCCCTGGCCAGCAGCCCCAGGCTGGCTC	900
257	Y K E G E R D F L Q R P G Q Q P Q A G L	276
901	TCCCAGGCCAACTTCACCCCTGGGCCCTGTGAGCCCTCCAATGGGGCCAGTACAGGTGC	960
277	S Q A N F T L G P V S P S N G G Q Y R C	296
961	TACGGTGCACACAACCTCTCCTCCGAGTGGTCGGCCCCAGCGACCCCTGAACATCCTG	1020
297	Y G A H N L S S E W S A P S D P L N I L	316
1021	ATGGCAGGACAGATCTATGACACCGTCTCCCTGTCAAGCACAGCCGGCCCCACAGTGGCC	1080
317	M A G Q I Y D T V S L S A Q P G P T V A	336
1081	TCAGGAGAGAACGTGACCCCTGCTGTCACTGGTGGCAGTTGACACTTCCTCTG	1140
337	S G E N V T L L C Q S W W Q F D T F L L	356
1141	ACCAAAGAACGGGCAGCCATCCCCACTGCGTCTGAGATCAATGTACGGAGCTCATAAG	1200
357	T K E G A A H P P L R L R S M Y G A H K	376
1201	TACCGGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCCGGGACCTACAGGTGC	1260
377	Y Q A E F P M S P V T S A H A G T Y R C	396
1261	TACGGCTCACGCAGCTCAACCCCTACCTGCTGTCAACCCAGTGAGCCCCCTGGAGCTC	1320
397	Y G S R S S N P Y L L S H P S E P L E L	416

FIG. 7B

## FcR-III

1321	GTGGTCTCAGGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCT	1380
417	V V S G H S G G S S L P P T G P P S T P	436
1381	GGTCTGGGAAGATACTGGAGGTTTGATTGGGGTCTCGGTGGCCTCGTCCTGCTGCTC	1440
437	G L G R Y L E V L I G V S V A F V L L L	456
1441	TTCCCTCCTCCTCTTCCTCCTCCGACGTAGCGTCACAGCAAACACAGGACATCTGAC	1500
457	F L L L F L L L R R Q R H S K H R T S D	476
1501	CAGAGAAAGACTGATTCCAGCGCTCTGCAGGGCTGCGGAGACAGAGCCAAAGGACAGG	1560
477	Q R K T D F Q R P A G A A E T E P K D R	496
1561	GGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTCTATGCTGCC	1620
497	G L L R R S S P A A D V Q E E N L Y A A	516
1621	GTGAAGGACACACAGTCTGAGGACGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAA	1680
517	V K D T Q S E D G V E L D S Q S P H D E	536
1681	GACCCCCACGCAGTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCC	1740
537	D P H A V T Y A P V K H S S P R R E M A	556
1741	TCTCCTCCTCCCCACTGTCTGGGAATTCTGGACACAAAGGACAGACAGGCAGAAGAG	1800
557	S P P S P L S G E F L D T K D R Q A E E	576
1801	GACAGACAGATGGACACTGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCC	1860
577	D R Q M D T E A A A S E A S Q D V T Y A	596
1861	CAGCTGCACAGCTTGACCCCTAGACGGAAGGCAACTGAGCCTCCTCCATCCCAGGAGTC	1920
597	Q L H S L T L R R K A T E P P P S Q E F	616
1921	GAGTCAGTCAGATCAGCATTGTGAGGCCCATCTCTACAAAAATAAAACCAGTCCGGCG	1980
617	E S V R S A L *	623

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Percent Similarity: 69.697

Percent Identity: 53.788

HMPAP73.aa x FCg2RBos.aa

**FIG. 8**

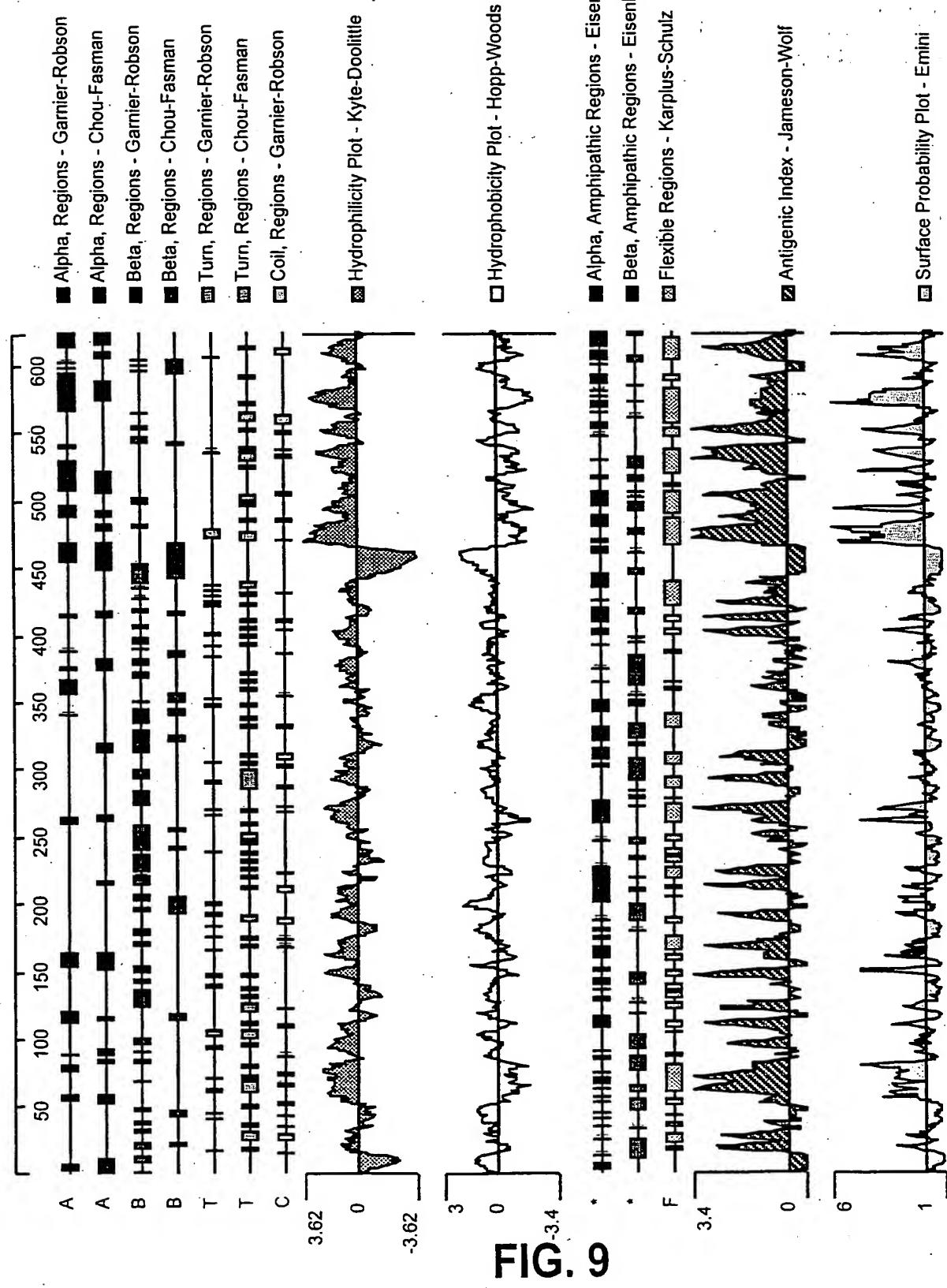


FIG. 9

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FcR-IV

1	GGAATTCCGGGAGGAGACGCCATGATCCCACTTCACGGCTCTGCTCTGCCCTGGGCTG	60
1	<u>M I P T F T A L L C L G L</u>	13
61	AGTCTGGGCCAGTACCCACATGCAGGCAGGGCCCTCCCCAAACCCACCCCTCTGGGCT	120
14	<u>S L G P S T H M Q A G P L P K P T L W A</u>	33
121	GAGCCAGGCTCTGTGATCAGCTGGGGAACTCTGTGACCATCTGGTGTCAAGGGACCCCTG	180
34	E P G S V I S W G N S V T I W C Q G T L	53
181	GAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAAGCCCAGCACCCCTGGACAGACAGAAC	240
54	E A R E Y R L D K E E S P A P W D R Q N	73
241	CCACTGGAGCCAAGAACAAAGGCCAGATTCTCCATCCATCCATGACAGAGGACTATGCA	300
74	P L E P K N K A R F S I P S M T E D Y A	93
301	GGGAGATAACCGCTGTTACTATCGCAGCCCTGTAGGCTGGTCACAGCCCAGTGACCCCCCTG	360
94	G R Y R C Y Y R S P V G W S Q P S D P L	113
361	GAGCTGGTGATGACAGGAGCCTACAGTAAACCCACCCCTTCAGCCCTGCCAGTCCTCTT	420
114	E L V M T G A Y S K P T L S A L P S P L	133
421	GTGACCTCAGGAAAGAGCGTGAACCTGCTGTGTCAGTCACGGAGCCAAATGGACACTTTT	480
134	V T S G K S V T L L C Q S R S P M D T F	153
481	CTTCTGATCAAGGAGGGGAGCCATCCCCATCCCTACTGCATCTGAGATCAGAGCACGGAGCT	540
154	L L I K E R A A H P L L H L R S E H G A	173
541	CAGCAGCACCAAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGTGCACGGGGGACCTAC	600
174	Q Q H Q A E F P M S P V T S V H G G T Y	193
601	AGGTGCTTCAGCTCACACGGCTCTCCACTACCTGCTGTCAACACCCAGTGACCCCCCTG	660
194	R C F S S H G F S H Y L L S H P S D P L	213
661	GAGCTCATAGTCTCAGGATCCTGGAGGGTCCAGGCCCTCACCCACAAGGTCCGTCTCA	720
214	E L I V S G S L E G P R P S P T R S V S	233

FIG. 10A

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FcR-IV

721	ACAGCTGCAGGCCCTGAGGACCAGCCCCATGCCTACAGGGTCAGTCCCCACAGTGGT	780
234	T A A G P E D Q P L M P T G S V P H S G	253
781	CTGAGAAGGCAGTGGAGGACTGATCGGGGCTTGGTGGCTCCATCCTGCTTCTCC	840
254	L R R H W E V L I G V L V V S I L L L S	273
841	CTCCTCCTCTCCTCCAAACACTGGCGTCAGGGAAAACACAGGACATTGGCCAG	900
274	L L L F L L Q H W R Q G K H R T L A Q	293
901	AGACAGGCTGATTCCAACGTCCAGGGCTGCCAGGCCAGAGCCAAAGGACGGGGC	960
294	R Q A D F Q R P P G A A E P E P K D G G	313
961	CTACAGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGGAGAAAATTCTGTGCTGCCGTG	1020
314	L Q R R S S P A A D V Q G E N F C A A V	333
1021	AAGGACACACAGCTGAGGACGGGTGAAATGGACACTCGGCAGAGCCCACACGATGAA	1080
334	K D T Q P E D G V E M D T R Q S P H D E	353
1081	GACCCCCAGGCAGTGACGTATGCCAAGGTGAAACACTCCAGACCTAGGAGAGAAATGCC	1140
354	D P Q A V T Y A K V K H S R P R R E M A	373
1141	TCTCCTCCCTCCCCACTGTCTGGGAATTCTGGACACAAAGGACAGACAGGCAGAAGAG	1200
374	S P P S P L S G E F L D T K D R Q A E E	394
1201	GACAGACAGATGGACACTGAGGTGCTGCATCTGAAGCCCCCAGGATGTGACTACGCC	1260
395	D R Q M D T E A A A S E A P Q D V T T P	413
1261	GGCTGCACAGCTTACCCCTAGACAGAAGGCAACTGAGCCTCTCCATCCCAGGAAGGG	1320
414	G C T A L P S D R R Q L S L L H P R K G	433
1321	CCTCTCCAGCTGAGCCCAGTGTCTATGCCACTCTGGCCATCCACTAATCCAGGGGGACC	1380
434	P L Q L S P V S M P L W P S T N P G G T	453
1381	CAGACCCCCACAAGCCATGGAGACTCAGGACCCCAGAAGGCATGGAAGCTGCCTCCAGTAG	1440
454	Q T P Q A M E T Q D P R R H G S C L Q *	472
1441	ACATCACTGAACCCAGCCAGCCCCACCCCTGACACAGACCACTAGAAGATTCCGGAA	1500
1501	CGTTGGGAGTCACCTGATTCTGCAAAGATAATAATCCCTGCATTATC	1550

FIG. 10B

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Percent Similarity: 67.969 Percent Identity: 50.781

HMSHH46new.aa x FCg2RBos.aa

1 MIPTFTALLCLGLSLGPSTHMQAGPLPKPTLWAEPGSVISWGNSVTIWCQ 50  
| ||:..|||||||:| .::|||.::|||.::|||:|||.||||:|||  
1 MAPTLPA LLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVPLGSSVTILCQ 50  
.  
51 GTLEAREYRLDKEESPAPWDRQNPLEPKNFKRFSI PSMTEDYAGRYRCYY 100  
| . :....|:|||:...||: .|||.:|||. | .. |: ||||:| ..  
51 GPPNTKSFSLNKEGDSTPWNIHPSLEPWDKANFFISNVREQQAGRYHCSH 100  
.  
101 RSPVGWSQPSDPLELVMTGAYS.....KPTLSALPSPLVTSGKSVTLLC 144  
.|||:|||:|||:|||:|.. :|||. ||| |..|..|||:  
101 FIGVNWSEPSEPLDLLVAGEEPAGRLDRPSLSVRPSPSVAPGENVTLLC 150  
.  
145 QSRSPMDTFLLIKERAHPLLHLRSEHGAQQHQAEFPMSPVTSVHGGTYR 194  
|| .. ||||| || |||. |:|||:.... .|||.:|||||,|||||||  
151 QSGNRTDTFLSKEGAAHRPLRLRSQDQDGWYQAEFSLSPVTSAHGGTYR 200  
.  
195 CFSSHGFSHYLLSHPSDPLELIVSGSLEGPRPSPTRSVSTAAGPEDQPLM 244  
|:| .: ..||||:|||:|||.|||: |: . | |:  
201 CYRSLSTNPYLLSQPSEPLALLV.....ADYTMQNL 232  
.  
245 PTGSVPHSGLRRHWEVLIGVLVVSILLSLLLFLLQHWRQGKHRTLAQR 294  
. | ..|:||| :|: |: |:| ..|  
233 RMG.....LAASVLLLGILL.....CQARHDHGGAR 259  
295 QAD 297  
:|.  
260 EAA 262

**FIG. 11**

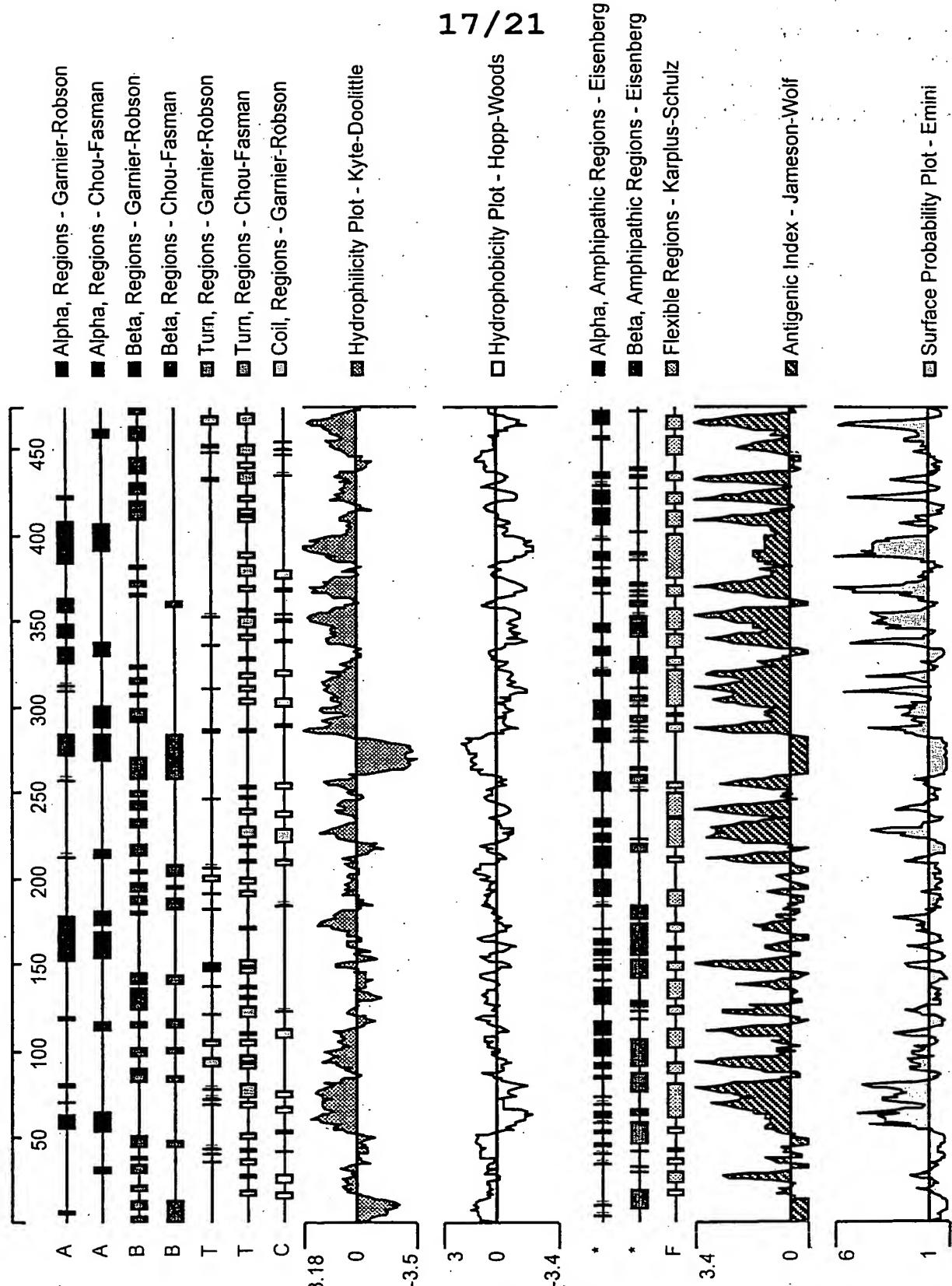


FIG. 12

1	GCAGGAATTGGCACGAGCAGAGCAGGGCAGTGGGAGGAGACGCCATGACCCCCATCC	60
1	<u>M T P I L</u>	5
61	ACGGTCTGATCTGCTCGGGCTGAGTCTGGGCCCCAGGACCCACGTGCAGGCAGGGCAC	120
6	<u>T V L I C L G L S L G P R T H V Q A G H</u>	25
121	CTCCCCAAGCCCACCCCTGGGCTGAGGCCAGGCTCTGTGATCATCCAGGAAAGTCCTGTG	180
26	L P K P T L W A E P G S V I I Q G S P V	45
181	ACCTCAGGTGTCAGGGAGCCTTCAGGCTGAGGAGTACCATCTATATAGGGAAAACAAA	240
46	T L R C Q G S L Q A E E Y H L Y R E N K	65
241	TCAGCATCTGGGTTAGACGGATAACAAGAGCCTGGGAAGAATGGCAGTCCTCCATCCA	300
66	S A S W V R R I Q E P G K N G Q F P I P	85
301	TCCATCACCTGGGAACACGCAGGGCGGTATCACTGTCAGTACTACAGCCACAATCACTCA	360
86	S I T W E H A G R Y H C Q Y Y S H N H S	105
361	TCAGAGTACAGTGACCCCTGGAGCTGGTGGTACAGGAGCCTACAGCAAACCCACCC	420
106	S E Y S D P L E L V V T G A Y S K P T L	125
421	TCAGCTCTGCCAGCCCTGTGGTACCTTAGGAGGGAACGTGACCCCTCCAGTGTCTCA	480
126	S A L P S P V V T L G G N V T L Q C V S	145
481	CAGGTGGCATTGACGGCTTCATTCTGTGTAAGGAAGGAGAAGATGAACACCCACAACGC	540
146	Q V A F D G F I L C K E G E D E H P Q R	165
541	CTGAACCTCCATTCCATGCCGTGGTGGTCCCTGGGCATCTTCTCCGTGGCCCCGTG	600
166	L N S H S H A R G W S W A I F S V G P V	185
601	AGCCCGAGTCGCAGGTGGTGTACAGGTGCTATGCTTATGACTCGAACCTCCATGTG	660
186	S P S R R W S Y R C Y A Y D S N S P Y V	205
661	TGGTCTCTACCCAGTGTCTGGAGCTCTGGTCCAGGTGTTCTAAGAACCCATCA	720
206	W S L P S D L L E L L V P G V S K K P S	225
721	CTCTCAGTGCAGCCAGGTCTATGGTGGCCCTGGGAGAGACCTGACCCCTCCAGTGTGTC	780
226	L S V Q P G P M V A P G E S L T L Q C V	245
781	TCTGATGTCGGCTACGACAGATTGTTCTGTATAAGGAGGGAGAACGTGACTTCCTCCAG	840
246	S D V G Y D R F V L Y K E G E R D F L Q	265

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841	CGCCCTGGTGGCAGCCCCAGGCTGGGCTCTCCCAAGGCCAACTTCACCCCTGGCCCTGTG	900
266	R P G W Q P Q A G L S Q A N F T L G P V	285
901	AGCCCCTCCCACGGGGGCCAGTACAGATGCTACAGTGCACACAACCTCTCTCCGAGTG	960
286	S P S H G G Q Y R C Y S A H N L S S E W	305
961	TCGGCCCCAGTGACCCCTGGACATCCTGATCACAGGACAGTTCTATGACAGACCCCT	1020
306	S A P S D P L D I L I T G Q F Y D R P S	325
1021	CTCTCGGTGCAGCCGGTCCCCACAGTAGCCCCAGGAAAGAACGTGACCCCTGCTGTGTCAG	1080
326	L S V Q P V P T V A P G K N V T L L C Q	345
1081	TCACGGGGCAGTCCACACTTCTGACCAAGGAGGGGGCAGGCCATCCCCACTG	1140
346	S R G Q F H T F L L T K E G A G H P P L	365
1141	CATCTGAGATCAGAGCACCAAGCTCAGCAGAACCCAGGCTGAATTCCGCATGGTCCTGTG	1200
366	H L R S E H Q A Q Q N Q A E F R M G P V	385
1201	ACCTCAGCCCACGTGGGACCTACAGATGCTACAGCTCACTCAGCTCCAACCCCTACCTG	1260
386	T S A H V G T Y R C Y S S L S S N P Y L	405
1261	CTGTCCTCTCCCAGTGACCCCTGGAGCTCGTGGTCTCAGCATCCCTAGGCCAACACCC	1320
406	L S L P S D P L E L V V S A S L G Q H P	425
1321	CAGGATTACACAGTGGAGAATCTCATCCGCATGGGTGTGGCTGGCTGGTCTGGTC	1380
426	Q D Y T V E N L I R M G V A G L V L V V	445
1381	CTCGGGATTCTGCTATTGAGGCTCAGCACAGCCAGAGAACCTACAAGATGCAGCCGG	1440
446	L G I L L F E A Q H S Q R S L Q D A A G	465
1441	AGTGAACAGCAGAGAGGACAATGCATCCTCAGCGTGGTGGAGCCTCAGGGACAGATCTG	1500
466	S E Q Q R G Q C I L Q R G G A S G T D L	485
1501	ATGATCCCAGGAGGCTCTGGAGGACAATCTAGGACCTACATTATCTGGACTGTATGCTGG	1560
486	M I P G G S G G Q S R T Y I I W T V C W	505
1561	TCATTTCTAGAGACAGCAATCAATATTGAGTGTAAAGGAACTGTCTGGGTGATTCTA	1620
506	S F L E T A I N I *	514
1621	GAAGATCATTAAACTGTGGTACATTTTTGTCTATG	1657

FIG. 13B

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Percent Similarity: 70.722 Percent Identity: 55.513  
HMAAB68.aa x FCg2RBos.aa

1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVIIQGSPVTLRCQ 50  
|.|.|..|:|||||:| ||:|||| :|||.:||||:|||: ||.||: ||  
1 MAPTLPAALLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVPLGSSVTILCQ 50  
  
51 GSLQAEYHLYRENKSASW.VRRIQEPGKNGQFPIPSITWEHAGRYHCQY 99  
|. ....: | :|..|..| ::. || ..:.| |..: ::|||||| .  
51 GPPNTKSFSLNKEGDSTPWNIHPSLEPWDKANFFISNVREQQAGRYHCSH 100  
  
100 YSHNHSSEYSDPLELVTGAYSKPTLSALPSPVTLGGNVTLQCVSQVAF 149  
: .|| |:||:|:|. |  
101 FIGVNWSEPSEPLDLLVAG..... 119  
  
150 DGFILCKEGEDEHPQRLNSHSHARGWSWAI FSVGVPSPSRRWSYRCYAYD 199  
:|.:||.  
120 .....EEPAGRLR..... 127  
  
200 SNSPYVWSLPSDLLELLVPGVSKKPSLSVQPGPMVAPGESLTQCVSDVG 249  
  
127 ..... 127  
  
250 YDRFVLYKEGERDFLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAH 299  
  
127 ..... 127  
  
300 NLSSEWSAPSPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQSRGQ 349  
|||||||.|| |.||||.||||||| ..  
128 .....DRPSLSVRPSPSVAPGENVTLLCQSGNR 155  
  
350 FHTFLLTKEGAGHPPHLRLRSEHQAQQNQAEFRMGPVTSAHVGTYRCYSSL 399  
.|||||.|||||:|.|:|||:|.. | |||.:||| |.||| |.||| .||  
156 TDTFLLSKEGAHRPLRLRSQDQDGWYQAEFSLSPVTSAHGGTYRCYRSL 205  
  
400 SSNPYLLSLPSDPLELVVSASLGQHPQDYTVENLIRMGVAGLVLVVLGIL 449  
|.|||||| |:||.||:|.. | |||:|||||:||: ||:|||  
206 STNPYLLSQPSEPLALLVA.....DYTMQNLIRMGLAASVLLLGIL 247  
  
450 LFEAQHSQRSLQDAAGS 466  
| :|.|..: : .|| |.  
248 LCQARHDHGGAREAARS 264

**FIG. 14**

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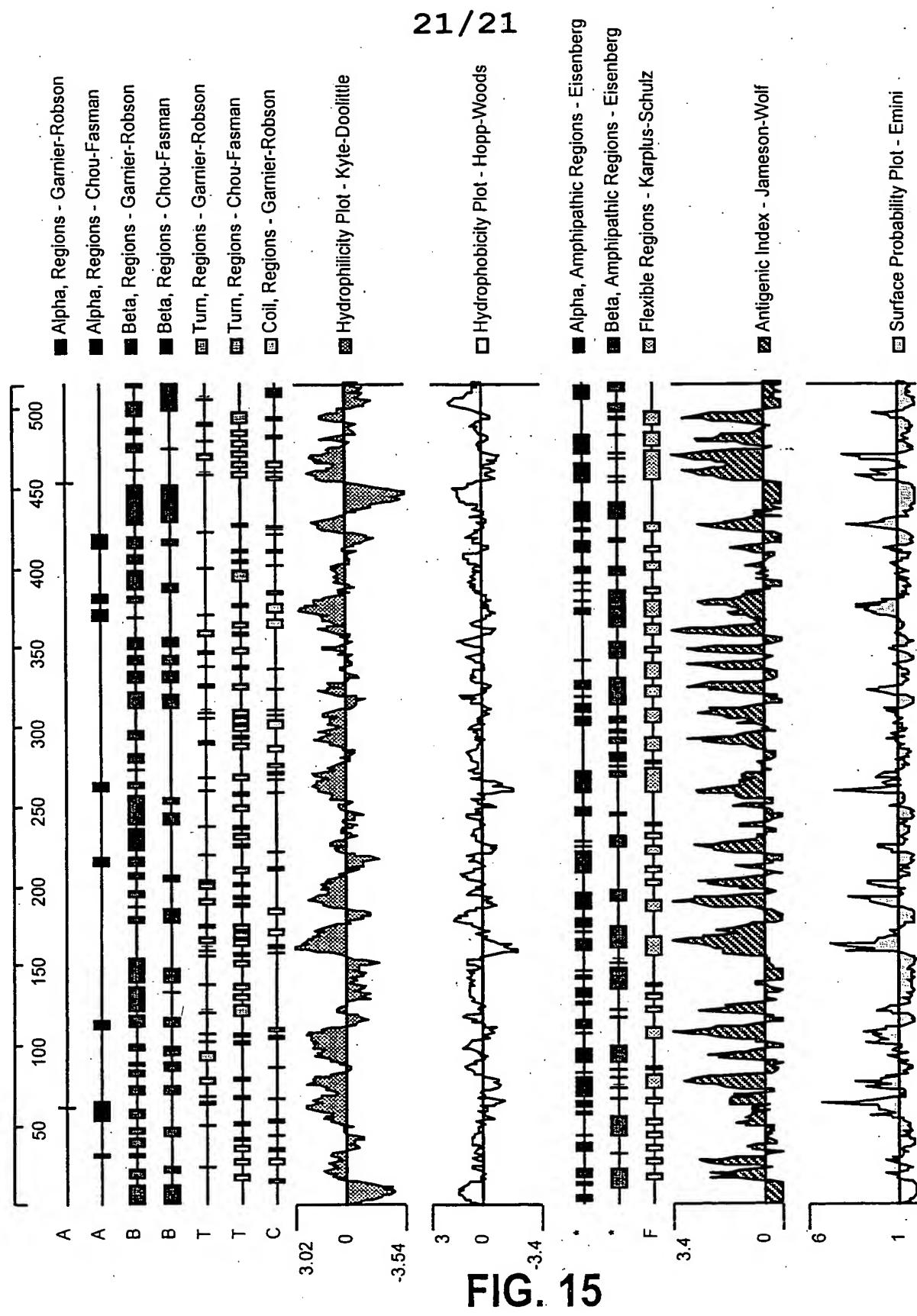


FIG. 15

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